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Lis	ting first 45 summaries						ALIGNMENTS

Abi 3938 Human che Abi 32242 Human imm Abi 37242 Human imm Abi 37242 Human imm Abi 370465 Chemicali Aba 6048 Drosophil Abi 6048 Drosophil Abi 52506 Human can Abi 52506 Human can Abi 52506 Human can Abi 525075 DNA encod Aax59975 DNA encod Aax59974 DNA encod Aax59974 DNA encod Aax1563 Encodes E Abi 32467 Human imm Abi 6148 Arabidops Abi 32467 Human imm Abx 6062 Human imm Abx 6062 Human imm Abx 6062 Human imm Abx 9920 Human sec Abi 3920 Human imm Abx 3920 Human imm Abx 3920 Human imm Abx 3920 Human imm Abx 3920 Human imm Abi 3920 Human imm Abi 3006 Human imm Abi 3000 Human imm Ab

ALIGNMENTS

PargCo; promoter; RNA synthesis; polypeptide synthesis; cell-free system; in vitro protein synthesis; ss. Nucleotide sequence of a fragment of the PargCo promoter. Ghochikyan A, Lecocq Geobacillus stearothermophilus. ACC43720 standard; DNA; 126 BP 27-JUL-2001; 2001EP-00402049. 27-JUL-2001; 2001EP-00402049. (revised)
(first entry) Sakanyan V, Snapyan M, (UYNA-) UNIV NANTES EP1279736-A1. 27-OCT-2003 11-AUG-2003 29-JAN-2003. ACC43720; RESULT 1 ACC43720

WPI; 2003-373763/36.

S Synthesizing RNA or a polypeptide from a DNA template comprises adding the reaction mixture the DNA template comprising a promoter with a UP element and encoding the desired protein and purified alpha subunit of the RNA polymerase.

Disclosure, Fig 1; 35pp; English.

The present sequence represents a fragment of the Bacillus stearothermophilus PargCo promoter. The PargCo promoter was used to construct recombinant DNA templates to drive protein synthesis in a cellfree system in the method of the invention. The specification describes a method of RNA or polypeptide synthesis from a DNA template. The method comprises providing a cell-free system enabling RNA or polypeptide

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RESULT 3
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synthesis from a DNA template comprising a promoter with at least one UP element, and recovering the synthesized RNA or polypeptide. The method is useful for synthesizing RNAs or polypeptides from a DNA template. The RNA produced from the method is useful as an mRNA for in vitro protein synthesis, as hybridization probes in diagnostic assays, as substrates for analysing processing reactions or RNA splicing, and for the production of specific proteins of interest, such as antigens for vaccines. (Updated on 27-OCT-2003 to standardise OS field)
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Pred. No. 1e-20;
Mismatches 0; Indels 0;
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100.0%; Pred. No. --
0; Mismatches
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ABL05742 Btandard; cDNA; 4663 BP.
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genes from Drosophila and
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P-PSDB; ABB61639.
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                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                           27 AAATCCTCGAAAATTATTAAATATACATTTGATTTTTATTATACAGTATTATAATGAG
printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                        36; Indels
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Pred. No. 21;
0; Mismatches
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Pred. No. 7.6;
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62.5%;
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Best Local Similarity 62.5.
Each Local Similarity 62.5.
Conservative
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29-AUG-2002
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2000US-0230438P.
2000US-0231243P.
2000US-0231243P.
2000US-0231244P.
2000US-0231413P.
2000US-0231414P.
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2000US-0231968P.
2000US-0232397P.
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2000US-0232399P.
2000US-0232400P.
2000US-0232401P.
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2000US-0237037P.
2000US-0237038P.
2000US-0237039P.
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2000US-0241221P.
2000US-0241785P.
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2000US-0246477P.
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2000US-0246528P.
2000US-0246532P.
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2000US-0236369P.
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2000US-0249213P
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
13-OCT-2000;
20-OCT-2000;
20-OC
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14-SEP-2000;
14-SEP-2000;
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17-NOV-2000;
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12-SEP-2000;
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiniflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
            AAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTTATTATACAGTATTATAAT 83
                                                                                                                                                                                                                                                                           Human musculoskeletal system related polynucleotide SEQ ID NO 2663
                                                                        GAGAACTACATGAGGCATACGGGTGAGGGGGAACATGATGAA 125
                                                                                                     GAAAAGTATCATTTAATAATTAACGGGAGGGGTTAGGATGAA 118
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AAL36298 standard; DNA; 6112 BP
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2000US-0186350P.
2000US-019634P.
2000US-0190076P.
2000US-020515P.
2000US-020515P.
2000US-0214886P.
2000US-0214886P.
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2000US-0214887P.
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2000US-0225214P.
2000US-0225266P.
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2000US-0225447P.
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2000US-0225758P.
2000US-0225759P.
2000US-0226279P.
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2000US-0220964P.
2000US-0224518P.
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2000US-0229343P
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24 - FEB - 2000;

15 - MAR 2000;

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17 - MAR 2000;

19 - MAR 2000;

10 - JUL 2000;

28 - JUL 2000;

20 - JUL 2000;

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21 - JUL 2000;

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24 - JUL 2000;

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11 - JUL 2000;

14 - JUL 2000;

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19 - AUG - 2000;

22 - AUG - 2000;

22 - AUG - 2000;

22 - AUG - 2000;
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AAL36297/c
ID AAL36297 standard; DNA; 6112 BP.
                                                                AAL36297;
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                                                         17-NOV-2000; 2000US-0249217P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-024926F.
17-NOV-2000; 2000US-024926P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-025103P.
18-DEC-2000; 2000US-025119P.
18-DEC-2000; 2000US-025119P.
18-DEC-2000; 2000US-0251186P.
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05-JAN-2001; 2001US-0259678P.
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les 57; Conservative
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                    Human musculoskeletal system related polynucleotide SEQ ID NO 2662
                                                                                                                                                                                                                2000US-0179065P.
2000US-0180628P.
2000US-0186350P.
2000US-0189874P.
2000US-0199123P.
2000US-0199123P.
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2000US-020545P.
2000US-0205467P.
2000US-0205467P.
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2000US-0205467P.
2000US-0218290P.
2000US-0217487P.
2000US-0217487P.
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                                   08-JAN-2002 (first entry)
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07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                          Homo sapiens.
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18-APR-2000;
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2000US - 0231968P
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2000US - 0232400P
2000US - 0233061P
2000US - 0233064P
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2000US - 0233064P
2000US - 0233065P
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2000US - 0234997P

2000US - 0235494P

2000US - 0235814P

2000US - 0235836P

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2000US - 023680ZP

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08-NOV-2000;
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The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids proteins, antibodies and cant)squares are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urgogenital, (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid archititis and ulcerative collitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases concertal, fungal and parastic infections Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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re-vascularisation; thrombosis; arteriosclerosis; mineral content;
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              01-DEC-2000; 2000US-0250160P.

01-DEC-2000; 2000US-0250391P.

05-DEC-2000; 2000US-0251030P.

05-DEC-2000; 2000US-0251988P.

06-DEC-2000; 2000US-02519F.

06-DEC-2000; 2000US-025186P.

08-DEC-2000; 2000US-025186P.

08-DEC-2000; 2000US-025186P.

08-DEC-2000; 2000US-025186P.

08-DEC-2000; 2000US-025186P.

08-DEC-2000; 2000US-025186P.
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1D ABX55
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AC ABX55
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DT 26-FF
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DB CDNA
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KW Gene
KW Te-vv
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cardiovascular condition; wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; AIDS-related complex; chondrocyte growth; bone regeneration; periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; open transplant; cell differentiation; bdy height; weight; hair colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; biorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; hormone level; endocrine level; appetie; libido; memory; stress; storage capability; fat content; libid content; protein content; carbohydrate content; vitamin content; cofactor content; 2000US-0225270P. 2000US-0225447P. 2000US-0229345P. 2000US-0234223P. 2000US-0234274P. 2000US-0234997P. 2000US-0235834P. 2000US-0236327P. 2000US-0236367P. 2000US-0236368P. 17-JAN-2001; 2001US-00764877 2000US-0217487P. 2000US-0217496P. 2000US-0218290P 2000US-0220963P 2000US-0229509P 2000US-0236369P 2000US-0236370P 2000US-0237038P nutritional component US2002147140-A1. 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; Homo sapiens. 05-SEP-2000; 29-SEP-2000; 29-SEP-2000; 01-SEP-2000; 21-SEP-2000; 25-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 02-OCT-2000; 14-AUG-2000; 21-SEP-2000; 29-SEP-2000; 10-OCT-2002

2000US-0251869P.

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The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metaseases, in animals or humans. The nucleic acid; stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, and other cardiovascular conditions such as thrombosis, arteriosclerosis, and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as Alzheimer's disease, Parkinson's disease, and AlDs-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or periodontal regeneration and aid in tissue transports or certivate hair-forming cells and promotes melanocyte growth; growth; prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates of monthly prevents hair loss, since FGF family members of ransplantation or for supporting cells und promotes melanocyte growth; stimulates induces tissue of mesodermal origin to differentiate or early embryos; induces tissue of mesodermal origin to differentiate in early embryos; induces tissue of mesodermal origin to differentiate in early embryos; concerts such as, body height, weight, hair colour, eye colour, exten or atter or physical state by influencing biorhythms, caricadic riviting state by influencing biorhythms, aricadic riviting state by influencing biorhythms, caricadic riviting state by influencing biorhythms, aricadic rapportive capabilities, hormonal or endocrine levels, appetite, libid, memory, or stress; increases or decreases storage capabilities, concert, vitamine, minerals, coffectors or other nutritional critical state or physical state by influencing propermines. This sequence encodes a novel human musculos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2667 ggaaaaaagagracacraacgacraaarggararraarrigraraargraccraar 2608
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                                                                                                                                                                                                        Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.6%; Score 36; DB 8; Length 6112; 62.0%; Pred. No. 29; tive 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140
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                                                                                                                                                                                                                                                                              Disclosure, SEQ ID NO 2662; 321pp; English.
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nes 57; Conservative
                                                                                                                Rosen CA, Ruben SM,
                                                                                                                                                            WPI; 2003-128199/12
                                                                 (BARA/) BARASH S C.
              (ROSE/) ROSEN C A. (RUBE/) RUBEN S M.
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Matches
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Gene; se; musculoskeletal system antigen; cancer; metastasis;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

re-vascularisation; thrombosis; arteriosclerosis; mineral content;

weardiovascular condition; wound; injury; burn; angiogenesis; ulcer;

we cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;

we neurodegenerative tissue repair; limb regeneration; neuronal growth; angiogenesis; chondrocyte growth; bone regeneration;

we related complex; chondrocyte growth; bone regeneration;

we relationcyte growth; hair loss; melanocyte growth; cell proliferation;

we cell growth; organ transplant; cell differentiation; body height; weight;

whair colour; eye colour; skin; percentage of adipose tissue;

pigmentation; cosmetic surgery; metabolism; blorhythm; caricadic rhythm;

depression; tendency for violence; pain; reproductive capability;

whormone level; endocrine level; appetite; libid; memory; stress;

storage capability; fat content; lipid content; protein content;

warbohydrate content; vitamin content; cofactor content;
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2000US - 0228924P
2000US - 0229343P
2000US - 0229343P
2000US - 0229345P
2000US - 0229345P
2000US - 0229345P
2000US - 0229513P
2000US - 0231413P
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2000US - 023423P
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2000US - 0234834P
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2000US-0225447P.
2000US-0225757P.
2000US-0225758P.
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2000US-0217487P.
2000US-0217496P.
2000US-0218290P.
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2000US-0244617P
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                                                                                                                                                                                                                    nutritional component
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14-AUG-2000;
22-AUG-2000;
30-AUG-2000;
01-SEP-2000;
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The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metasetases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions, and ulcers, stimulates analogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerations, such as, Alzheimer's disease, Parkinson's disease, and AlDS. conditions, such as, Alzheimer's disease, Parkinson's disease, and AlDS. crelated complex; stimulates chondrocyte growth, thus they can be used to chance bone and pariodontal regeneration and aid in tissue transports or certain acid and promotes melanocyte growth stimulates cortivate hair-forming cells and promotes melanocyte growth; stimulates crivate hair-forming cells and promotes melanocyte growth; stimulates of creation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, heamedamil origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, heamedamilorical inneas; modulates mammalian command or subgery; modulates mammalian metabolism; characteristics, such as, body height, weight, hair colour, eye colour, skiin, percentage of adipose tissue, pigmentation, size, and shape (e.g., capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, modulates mammalian compenses increases
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                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 2663; 321pp; English.
                                                                                                                                                                                        Barash SC;
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
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ID ADJ30035 standard; DNA; 6112
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Matches 57; Conservative
                                                                                                                                                                                        Rosen CA, Ruben SM,
                                                                                                                                                                                                                                      WPI; 2003-128199/12.
                                                                                                                (RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                        (RUBE/) RUBEN S M.
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2000US-023405P.
2000US-023423P.
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2000US-023439P.
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2000US-023439P.
2000US-023439P.
2000US-0235336P.
2000US-0235336P.
2000US-0235336P.
2000US-0235336P.
2000US-023636P.
2000US-023636P.
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2000US-023636P.
2000US-024178F.
2000US-024180P.
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2000US-024180P.
2000US-024178F.
2000US-024178F.
2000US-024178F.
2000US-024652P.
2000US-024921P.
2000US-024929P.
2000US-024929P.
2000US-024929P.
2000US-0250399P.
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2000US-0251856P.
2000US-0251868P.
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
14-SEP-2000;
11-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
27-SE
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08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
     musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis; gene therapy; vaccine; human; ds.
                                                           Human musculoskeletal system-associated genomic DNA - SEQ ID 2662
                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0179065P

2000US-0180628P

2000US-018064P

2000US-0189874P

2000US-0190076P

2000US-0190076P

2000US-029467P

2000US-0209467P

2000US-0209467P

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2000US-0227182P.
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2000US-0229287P.
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2000US-0231413P.
2000US-0231414P.
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2000US-0233063P
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14-AUG-2000;
22-AUG-2000;
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31-AUG-2000;
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2000US-0217496P.
2000US-0218290P.
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2000US-0220964P.
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associated mucleic acid molecule. The nucleic acid of the invention
demonstrates cytostatic and osteopathic activities and may be useful for
preparing a medicament for preventing, treating or ameliorating a medical
condition such as cancer of the musculoskeletal tissues or osteoporosis,
possibly via gene therapy or vaccine production. The current sequence is
that of the human musculoskeletal system-associated genomic DNA of the
invention. The current sequence is not shown within the specification per
se but is available on the USPTO web-site
                                                                                                                                           New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer of musculoskeletal tissues or osteoporosis.
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gene therapy; vaccine; human; ds.
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Pred. No. 29;
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ID ADJ30036 standard; DNA; 6112 BP
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2000US-018464P.
2000US-0186350P.
2000US-0189874P.
2000US-0190076P.
         08-DEC-2000; 2000US-0251989P-
08-DEC-2000; 2000US-0251990P-
11-DEC-2000; 2000US-0254097P-
05-JAN-2001; 2001US-0259678P-
17-JAN-2001; 2001US-02678P77-
2000US-0251869P
                                                                            (HUMA-) HUMAN GENOME SCI INC
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62.0%;
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Best Local Similarity 62.0°
Matches 57; Conservative
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18-APR-2000;
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2000US-0241809P
2000US-0244617P
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2000US-0246474P
2000US-0246475P
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from base 1600001 (Listeria monocytogenes EGD-e genor LOCUS ABA03041 Accession Aba03041
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preparing a medicament for preventing, treating or ameliorating a medical condition such as cancer of the musculoskeletal tissues or osteoporosis, possibly via gene therapy or vaccine production. The current sequence is that of the human musculoskeletal system-associated genomic DNA of the invention. The current sequence is not shown within the specification per se but is available on the USPTO web-site http:seqdata.uspto.gov/sequence.html?DocID=20040009488.
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into 30 fragments
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les 57; Conservative
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ABA03041 16/C

Continuation (17 of 30) of

WP Fragment Name

WP ABA03041 00

WP ABA03041 01

WP ABA03041 02

WP ABA03041 02

WP ABA03041 06

WP ABA03041 06

WP ABA03041 10

WP ABA03041 12

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Mouse Cd28 carcinoma associated gene, SEQ ID NO:1505.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABG6671-ABG67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for single-nucleotide polymorphisms, in angiogenesis-related genes, for adiagnosis and treatment of eye diseases, proliferative retinopathy, neowascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and crohn's disease. Note: The sequence datas for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AGAAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTATTTTATACAGTATTAT 80
                                                                                                             Human; angiogenesis; methylation; eye disease; glaucoma; tumour;
inflammation; rheumatodi arthritis; diabetic retinopethy; antiulcerds;
macular degeneration; inflammatory bowel disease; Crohn's disease;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g. in
diagnosis or treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
28.3%; Score 35.6; DB 6; Length 5237;
Best Local Similarity 67.6%; Pred. No. 35;
Matches 50; Conservative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5237 BP; 1086 A; 75 C; 1422 G; 2654 T; 0 U; 0 Other;
                                                                                        Human angiogenesis associated polynucleotide SEQ ID NO 138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 138; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA02987 standard; DNA; 27587 BP
ABQ67108/c
ID ABQ67108 standard; DNA; 5237 BP.
                                                                                                                                                                                                                                                                      06-DEC-2001; 2001WO-EP014320.
                                                                                                                                                                                                                                                                                               06-DEC-2000; 2000DE-01061338.
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                                                             (first entry)
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                                                                                                                                                                   antiarteriosclerotic; ds.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-500450/53.
                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                    WO200246454-A2.
                                                              28-AUG-2002
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                                                                                                                                                                                                                                            13-JUN-2002
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                                     ABQ67108;
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ID ADAC
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to caid sequences from mouse and human (ADA01482-ADA03094), and to crecombinant carcinoma associated proteins (CAP) encoded by them. Them. The invention also encompasses expression vectors and host calls comprising a cinvention also encompasses expression vectors and host calls comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically compared to the protein, and a blockip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using concepency retroviruses, which insert into the genome of the host organism or transporting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host proteonnoogenes. The CA nucleic acid sequences can be used to diagnose carcinoma (especially breast cancer, prostate cancer, lymphoma or expression or a propensity to carcinoma by determination of the sequence carcinoma carcinoma protein and in screening and antibodies are also useful as therefore of the invention. Note: The complete sequence date for this sequence of the invention. Note: The complete sequence date for this sequence of the printed specifically claimed murine CA nucleic acid sequence for the printed specification, but was obtained consequence of the printed specification, but was obtained consequence and protein and specification, but was obtained consequence and protein sequences.
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prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27587 BP; 7952 A; 5475 C; 5626 G; 8534 T; 0 U; 0 Other;
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Local Similarity 63.5%; Pred. No. 45;
nes 54; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1505; 245pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-DEC-2002; 2002WO-US041414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-DEC-2001; 2001US-00035832.
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                                                                                                                                                                                                                                                                                              The invention relates to a recombinant nucleic acid comprising a nucleotide sequence selected from any of the fully defined carcinoma-associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; carcinoma associated nucleic acid; CA nucleic acid; gene; ds; carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
                                                                                                                                                                         New recombinant nucleic acid comprising a nucleotide sequence of ar
the carcinoma-associated (CA) genes, useful for screening for drug
candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia or lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27587 BP; 7952 A; 5475 C; 5626 G; 8534 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 27587;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine carcinoma associated (CA) nucleic acid #127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7499 CCAAGGAATTCATGTGTAGGAAATC 7523
                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 253; 983pp; English
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Local Similarity 63.5%;
Les 54; Conservative 0
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                30-NOV-2001; 2001US-00997722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-2001; 2001US-00997722
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                                                        (SAGR-) SAGRES DISCOVERY
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                                                                                                Engelhard
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                                                                                                                                      WPI; 2003-513603/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004072154-A1
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                                                                                                Morris DW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 TCGAAAATTATTAAATATACATTTGATTTTTATTTTTATACAGTATTATAATGAGAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                       cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27587 BP; 7952 A; 5475 C; 5626 G; 8534 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.1%; Score 35.4; DB 10; Length 27587; Best Local Similarity 63.5%; Pred. No. 45; Matches 54; Conservative 0; Mismatches 31; Indels 0;
                                                          cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancers, neoplasm, adenocarcinoma, or sarcomas.
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23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00937722.
20-DEC-2001; 2001US-00034650.
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                                                                                                                                          WO2003008583-A2
Mouse Cd28 gene
                                                                                                                                                                                                                       26-DEC-2001;
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                                         mouse; ds;
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Claim 1; SEQ ID NO 253; 29pp; English

also relates to a host cell comprising a recombinant nucleic acid or expression vector, an expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for drug candidates, a method of screening for a bicactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a method of screening for a bicactive agent capable of modulating the activity of a CAP, a method of evaluating the effect of a candidate carcinoma drug, a method of flagnosing carcinoma, a method of the activity of a CAP, a method of treating carcinoma, a method of the activity of a CAP, a method of treating carcinoma, a method of propensity to carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a call sample from the patient and determining alterations in the carcinomas comprises administering to a patient an inhibitor of CAP.

Neutralising the effect of a CAP comprises contacting an agent specific for the CAP. The polypeptide specifically binds to the protein encoded by the nucleic acid. It comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acids are useful for preparing a composition for diagnosing or treating carcinoma e.g., leukaemia or lymphoma. This sequence represents a murine carcinoma associated (CA) nucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at expression or activation of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of one or more genes comprising the nucleic acid sequence in a first tissue type of a first individual and comparing the expression of the gene from a second normal tissue type from the first individual, where a difference in the expression indicates that the first individual has carcinoma. A method of inhibiting the activity of a CAP comprises binding an inhibitor to the CAP. Treating invention relates to new recombinant nucleic acids. seqdata.uspto.gov/sequence.html

Sequence 27587 BP; 7952 A; 5475 C; 5626 G; 8534 T; 0 U; 0 Other;

Query Match 28.1%; Score 35.4; DB 12; Length 27587; Best Local Similarity 63.5%; Pred. No. 45; Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps

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7439 rcaaaacrarararararararrirrrrrrrrrrrrrracracragacregaacreg 33 TCGAAAATTATTAAATATACATTTGATTTTTATTATACAGTATTATAATGAGAACTAC 92 g ઠે

93 ATGAGGCATACGGGTGAGGGGGAAC 117

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                                                         AL451002 Homo sapi
AE013064 Thermoana
AC13021 Macaca mu
CR382400 Plasmodiu
AK416348 Sequence
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AE017327 Listeria
AC16042 Arabidops
AC144983 Xenopus t
AC104042 Homo sapi
AC1544983 Medicago
AC125478 Medicago
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AC137069 Luman DNA
CR513788 Danio rer
AL13728 Human DNA
CR647834 Danio rer
AL691416 Mouse DNA
CR847834 Danio rer
AL691416 Mouse DNA
CR84635 Streptoco
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Extremophiles 3 (1), 21-28 (1999)
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Extremophles 3 (1), 29-34 (1999)
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Horikoshi, K.
Sequence analysis of a 32-kb region including the major ribosomal
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Reidentification of facultatively alkaliphilic Bacillus sp.
to Bacillus halodurans
Biosci. Biotechnol. Biochem. 63, 943-945 (1999)
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Bacillus halodurans C-125
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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EXTREMOPHILES IN DEEP-SEA ENVIRONMENTS: 249-284;
Springer-Verlag (1999)
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CQ578096 Sequence
AC018035 Drosophil
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AC007539 Drosophil
AE007753 Drosophil
AE007789 Drosophil
AE077831 Human DNA
AC055099 Rattus no
BX640454 Zebrafish
AE017011 Bacillus
AL923356 Plasmodiu
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BX936455 Zebrafish
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URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,
Tel:81-468-67-3895, Fax:81-468-66-6364)
Location/Qualifiers
protein gene clusters from alkaliphilic Bacillus sp. strain C-125
Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
99209008
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Takami, H. and Takaki, Y.
Direct Submission
Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and Technology Center, Deep-sea Microorganisms Research Group, 2-15
Natsushima, Yokosuka, Kanagawa 237-0061, Japan
                                                                                                                             Takami, H., Masui, N., Nakasone, K. and Horikoshi, K. Replication origin region of the chromosome of alkaliphilic Bacillus halodurans C-125
Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL, Sw.; SWISSPROT; Tr., TREMBL; WD:, WORMPEP; Information the tree of the found at the found 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSNQEERDFFTDLMFGRPPESTDVAEENPQESTSGSTVEETKTE
GETKQEETNAAPALPLFFEQMEHIFRLAQSLGPALKSLSPYVKTIQQLISQQKKD"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MNVYTHGPYYRQYGYIGTGERFYPAVLPFLAGLAVGPLLFGGKP
YGGYGPAYGPSYGPNFGPNYGPNFGPMYGPPSQPPFGYYK"
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Zebrafish DNA sequence from clone DKEY-199112 in linkage group 20,
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyptiniformes; Cyprinidae; Danio.
1 (bases 1 to 123707)
Phillimore, B.
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Submitted (10-JUN-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 30, 2004_this sequence version replaced gi:47776037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep_Clone-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AAAAAAATCCTCGAAAATTATTAAATATATACATTTGATTTTATTTTATACAGTATTATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40.4; Pred. No. 10;
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Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                      /transT_table=11
/protein_id="BAB06604.1"
/db_xref="G1:10175507"
                                                                             complement (5903. .6157)
                                                                                                                                               complement (5903.
/gene="BH2885"
/note="BH2885
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                                                                                                                                                                                                                                                                                                   /codon_start=1/transT_table=
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Danio rerio
                                                                                                                    /gene="BH2885
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Best Local Similarity
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BX936455
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Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see thttp://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-199112 is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8300 AATATCATTGAAGATTTTTAAACAAACAATTTATGTTATTTTTATAAATTATTTTAATGA 8359
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Direct Submission

Submitted (06-JUN-2004) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. B-mail enquiries:

zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jun 7, 2004 this sequence version replaced gi:46878815.

Center: Wellcome Trust Sanger Institute
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Zebrafish pUC subclones occasionally display inconsistency over length of mononucleotide A/T runs and conserved TA repeats. Wher this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 AAAATCCTCGAAAATTATTAAATATACATTTGATTTTATTATTACAGTATTATAATGA
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Chemistry: Dye-terminator: 100% of reads
Consensus quality: 152706 bases at least Q40
Consensus quality: 152778 bases at least Q30
Consensus quality: 152797 bases at least Q30
Insert size: 152861; sum-of-contigs
Insert size: 158661; als error; agarose-fp
Quality coverage: 7.35x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gap between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 123707;
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Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 152961)
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BX957289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.1%; Score 39.2; D 78.3%; Pred. No. 22; ive 0; Mismatches
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Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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HTG; HTGS PHASE1; HTGS CANCELLED.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="DanioKey"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="DKEY-199112"
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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BX957289
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LSHHLSTTPNTAFMGNVTQKPDVKRFTKDGAVFTDGSTESFDHVMFCTGYKYTFPČLS
TDVGVQVDIDNSFVQPLMKHGININHPTMAFVGLDFRNTZPTHIPDMQVPFTLKFFTGQRK
FPSREQMIADLEQEIGERWGCGVRQKKAHQMGERQFVYYNELASIAGIENIKPVIHK
IMKOGGKKTIFELDFYRSNKYTILDDENFLKNGEAIV"
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LRSYAEHFKVKPHIKLOHEVIRVRPRLDDWEVYVWDHSTDTCDPVYYDFVYVCNGHYT
BPDLPBVEGLDLFEGNKMHSHLYRKADKFKDARVLIIGAGPSGMDITNHVRLAAKOVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1257 AAATCCTGAAAGGTTTATATATATCCACATAAAACTTTTGTTTTTATAAATGATAGAAGCTT 1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MIKTSVDKRRVCVIGAGTAGLCALKNSLEAGLDAVAYERGTEIG
                                                                                                           2 (bases 1 to 2307)
Scharf, M.E., Scharf, D.W., Bennett, G.W. and Pittendrigh, B.R.
Direct Submission
Submitted (11-0CT-2001) Entomology, Purdue University, 1158 Smith
Hall, West Lafayette, IN 47907-1158, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                               /map="ZR; 42B2-3"
join(<1. 46,108. .270,329. .518,629. .800,1474. .2012,
2128. .2307)
/product="flavin-containing monooxygenase FWO-2"
join(1. .46,108. .270,329. .518,629. .800,1474. .2012,
2128. .2307)
/mote="similar to GG3174 product of GenBank Accession
Number AAF2734; NAD- and FAD-binding protein; putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter,J.C., Adams,M., Li,P.W. and Myers,E.W.
Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 011042-A 5854 27-SEP-2001;
PE Corporation (NY) (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 AAAICCICGAAAAITAITAAAIAIACAITIGAITITIAITITIAIACAGTAITATAAIGAG
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
              Scharf,M.E., Scharf,D.W., Bennett,G.W. and Pittendrigh,B.R. Catalytic activity and expression of two flavin-containing monooxygenases from Droscophila melanogaster Arch. Insect Biochem. Physiol. 57 (1), 28-39 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="flavin-containing monooxygenase FMO-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 2307;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38.4; DB 3; Length 2 Pred. No. 60; 0; Mismatches 36; Indels
                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="Canton-S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1317 TACTACATGAGCCATCCATGATATATGTTACATGAT 1352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAL27708.1"
/db_xref="G1:16751750"
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62.5%;
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                   Length 152961;
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                1 149984: contig of 149984 bp in length 5 150964; gap of 100 bp 5 152951: contig of 2877 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                                                                                                                                                                                           /clone_lib="CHORI-211"
1.1459884
/note="assembly_fragment:02029.0"
150085. .152961
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                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                 31.1%; Score 39.2; I
78.3%; Pred. No. 21;
                                                                                                             /organism="Danio rerio"
/mol type="genomic DNA"
/db xref="taxon:7955"
/clone="CH211-232C6"
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                                                                                             . .152961
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Best Local Similarity 78.3
Matches 47; Conservative
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nes 55; Conservative
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    be preserved
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Continuation (6 of 14)
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PFMAL7P1 02
PFMAL7P1 03
PFMAL7P1 04
PFMAL7P1 04
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PFMAL7 P1 07
PFMAL7 P1 08
PFMAL7 P1 09
PFMAL7 P1 10
PFMAL7 P1 11
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PFMAL7P1 05/c
WPCOMMENT
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Sequence split into
PFWAL/P1_06
PFWAL/P1_07
PFWAL/P1_08
PFWAL/P1_09
PFWAL/P1_10
PFWAL/P1_11
PFWAL/P1_12
PFWAL/P1_12
Continuation (14 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFMAL7P1 00
PFMAL7P1 01
PFMAL7P1 02
PFMAL7P1 03
PFMAL7P1 04
PFMAL7P1 04
PFMAL7P1 05
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PFMAL7P1_08
PFMAL7P1_09
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PFMAL7P1 11
PFMAL7P1 12
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AC007624/c
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                                                                                                                                                                                                                                                                                                                                            41909 bp DNA linear HTG 09-DEC-1999
, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                               2341 AAATCCTGAAAGGTTTATATATCCACATAAAACTTTTGTTTTATAAAATGATAGAAGCTT 2282
                                                                                                                                                                 27 AAATCCTCGAAAATTATTAAATATACATTTGATTTTATTTTTTATACAGTATTATAATGAG 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams, M. and Venter, J.C.

Direct Submission

Bubmitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,

Bockville, MD, USA

This sequence was identified as CDM:10213107 by the submitter.

For more information on this record e-mail to fly@celera.com.

* NOTE: This is a "working draft" sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                   Gaps
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AC018035
AC018035
AC018035
HTGS PHASE2.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, 1 (bases 1 to 41909)
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llarity 62.5%; Pred. No. 39;
Conservative 0; Mismatches 16. Trail
                                                                                                   Length 4663;
                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                             2281 TACTACATGAGCCATCCATGATATATGTTACATGAT 2246
                                                                                                                                                                                                                               87 AACTACATGAGGCATACGGGTGAGGGGGAACATGAT 122
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                                                                                                 DB 6;
                                                                                               30.5%; Score 38.4; D
llarity 62.5%; Pred. No. 54;
Conservative 0; Mismatches
                    Sp."
DNA"
   1. .4663
/organism="Drosophila
/mol_type="unassigned
/db_xref="taxon:7242"
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nes 60; Conserv
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PFMAL7P1 01
PFMAL7P1 02
PFMAL7P1 03
PFMAL7P1 04
PFMAL7P1 05
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of PFMAL7P1 from base 1200001 (AL844506 Plasmodium falciparum 3'
                                                                                                                            of PFMAL7P1 from base 1300001 (AL844506 Plasmodium falciparum 3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167062 bp DNA linear HTG 13-DEC-1999 Drosophila melanogaster chromosome 2 clone BACR10F15 (D621) RPCI-98 ***, 25 unordered pieces.
                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Meoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae; Drosophila.

1 (bases 1 to 167062)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
                                                                                                                                                                                                                         24 AAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTATTTTTTATACAGTATTATAAT
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                                                                                                                                                           Length 51552;
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                                                                                                                                                        Score 38.4; DB; Pred. No. 38; 0; Mismatches
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HTGS HTGS PHASE1.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                     9614 AATTATTATTGATCCATACTTGTGATG 9641
                                                                                                                                                                                                                                                                                        84 GAGAACTACATGAGGCATACGGGTGAGG 111
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64.8%;
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1 Similarity 64.8%;
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Continuation (13 of 14)
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Best Local Similarity
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AC007593/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (121-MX1-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Dec 13, 1999 this sequence version replaced gi:5670596. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as 'wing of the contigs are represented as 'runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will 'be be preserved.
                                                                                                                                                                                                                                                      Celniker, S. B., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.B., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lonotani, M.A., Maxda, P., Moshrefi, A.R., Moshrefi, M. Mixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Schi, H., Snir, B., Suyiskas, R.R., Man, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Richards, S., Sechi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
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6: contig of 970 bp in length
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Neopetra's Endopetrace, Article Decrea, Brachycera; Muscomorpha; Brydroides; Drosophilidae; Drosophila.

Ephydroides; Drosophilidae; Drosophila.

I (bases 1 to 173702)

Gelniker's E., Adam's D., Kronmiller'B., Tyler'D., Wan,K.H., Repers'Y. An,H., Baldwin,D., Banzon,J., Beeson,K.Y.; Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M., Ferrieras,S., Frise,E., Galle,R.F., Gargin,S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Saveri,J.S., Smith,H.O., Rubin,G.M. and Veneer,J.C.
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Drosophila melanogaster, chromosome 2R, region 42E-43A, BAC clone
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Celniker, S.B., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Caluiker, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Calle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 167062;
78928: gap of unknown length
106751: contig of 27823 bp in length
130045: contig of 27823 bp in length
130145: contig of 23214 bp in length
130125: gap of unknown length
165293: contig of 35168 bp in length
165599: contig of 256 bp in length
165679: gap of unknown length
165679: gap of unknown length
166687: contig of 608 bp in length
166687: gap of unknown length
167062: contig of 608 bp in length
167062: contig of 695 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38.4; DB 2; Length 16
Pred. No. 31;
0; Mismatches 36; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      1. .167062
/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="y; on bw sp"
/db_xref="taxon:7227"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="42E-43A"
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                          165374
165600
165680
165680
                                                                                                                        130046
130126
165294
                                                                  106752
106832
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Dietz,S.M., Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S.,
Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C.,
Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C.,
Gelbart,M.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z.,
Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J.,
Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J.,
Wei,M.H., Ibegwam,C., Jalali,M., Kalush,P., Karpen,G.H., Ke,Z.,
Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
Li,Z., Liang,Y., Lin,X., Mattel,B., Montosh,Y.C.,
Mizot,M.P., McPherson,D., Morkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Nusskern,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S.,
Pollard,J., Puri,V., Smith,T., Spier,E., Spradling,A.C.,
Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R.,
Weinstock,G.M., Weissenbach,J., Williams,S.M., WoodgefT,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
Zhong,F.N., Zhong,W., Zhu,S., Zhu,S., Sulth,H.O.,
Glbbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (06-SEP-2002) University of California Berkeley, 539 Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misra,S., Crosby,M.A., Mungall,C.J., Matthews,B.B., Campbell,K.S. Hradecky,P., Huang,Y., Kaminker,J.S., Millburn,G.H., Prochnik,S.B. Smith,C.D., Tupy,J.L., Whitfied,B.J., Bayraktaroglu,L., Berman,B.P., Bettencourt,B.R., Celniker,S.B., de Grey,A.D., Drysdale,R.A., Harris,N.L., Richter,J., Russo,S., Schroeder,A.J., Stu,S.Q., Stapleron,M., Yamada,C., Ashburner,M., Gelbart,W.M., Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 333736)
2 (bases 1 to 333736)
4 (bases, S.B., Wheeler, D.A., Kronmiller, B., Carlson, J.W.,
Halpern, A., Patel, S., Adams, M., Champe, M., Dugan, S.P., Frise, E.,
Hodgson, A., George, R.A., Hoskins, R.A., Laverty, T., Muzny, D.M.,
Nelson, C.R., Pacleb, J.M., Park, S., Pfeiffer, B.D., Richards, S.,
Sodergren, B.J., Svirskas, R., Tabor, P.E., Wan, K., Stapleton, M.,
Sutton, G.G., Venter, C., Weinstock, G., Scherer, S.E., Myers, E.W.,
Gibbs, R.A. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence Genome Biol. 3 (12), RESEARCH0079 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaminker, J.S., Bergman, C.M., Kronmiller, B., Carlson, J., Sylrakas, R., Patel, S., Frise, E., Wheeler, D.A., Lewis, S.E., Rubin, G.M., Ashburner, M. and Celniker, S.E. The transposable elements of the Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 systematic review
Genome Biol. 3 (12), RESEARCH0083 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euchromatin: a genomics perspective
Genome Biol. 3 (12), RESEARCH0084 (2002)
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AUTHORS
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MEDLINE
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AUTHORS
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Ephydroidea; Drosophilae; Drosophila.

I (bases 1 to 333736)

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Handerson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nalson, C.R., Gabor, G.L., Abril, J.F., Apbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Baxman, B.P., Bayaktaroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Buktis, K.C., Busam, D.A., Buller, H., Cadieu, E., Center, A., Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102329 AAATCCTGAAAGGTTTATATATACCACATAAAACTTTTGTTTTATAAAATGATAGAAGCTT 102270
                                                                                                                                                                                                                                                                                                                 Sequence submitted by:

Berkeley prosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.

Location/Qualifiers

1. 173702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                         Submitted (20-MAY-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA ON Mar 10, 2001 this sequence version replaced gi:7018749.
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2R, section 6 of 74 of the
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                     Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeliffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Syirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
pBACe3.6)"
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Pred. No. 31;
0; Mismatches 36; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2R"
/map="42E-43A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 AACTACATGAGGCATACGGGTGAGGGGGAACATGAT 122
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AE003789 AE002778 AE013599
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Best Local Similarity 62.5%;
Matches 60; Conservative
                                                                                                                                                                                          Direct Submission
                                                                                                                                                          Rubin, G.M.
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AE003789/c
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Prochnik, S.B.,

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DEFINITION
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                                                                    Direct Submission
Submitted (10-MAR-2004) FlyBase, Harvard University, Biological
Laboratories, 16 Divinity Avenue, Cambridge, MA 02138, USA
On Feb 14, 2003 this sequence version replaced gi:21626868.
Location/Qualifiers
                                                                                                                                                                                melanogaster"
Sciences Addition, Berkeley, CA 94720, USA 7 (bases 1 to 333736)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transposon="X-element{}713"
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/470. 7542
/locus_tag="TE19944"
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complement(21555.23451)
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    /locus tag="TE19942"
    /map="42A15-42A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transposon="GATE(}719"
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2283. .2997
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11077. 11685
10cus tag="TE19945"
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db_xref="FLYBASE:FBti0019945"
2638. .12835
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|db xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                         complement (1120. .1449)
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map="42A16-42A16"
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                                                     FlyBase
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Submitted (20-007-2011) Sanger Centre, Hinxton, Cambridgeshire, Calo 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerques(Banger.ac.uk Cone Oct 24, 2001 this sequence version replaced gi:16116426. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307209 AAATCCTGAAAGGTTTATATATCCACATAAAACTTTTGTTTTATAAAATGATAGAGCTT 307150
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Human DNA sequence from clone RPI1-108B14 on chromosome 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176577)
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Best Local Similarity 62.5%; Pred. No. 28;
Matches 60; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307149 TACTACATGAGCCATCCATGATATATGTTACATGAT 307114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 AACTACATGAGGCATACGGGTGAGGGGGAACATGAT 122
                                                                                                                                                                                                                                                                                                                                                                                                            /transposon="GATE()723"
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db_xref="FLYBASE:FBti0019950"
                               complement(27218. .27779)
/locus taq="TE19951"
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AL157831/c
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyaleberdi, V., Aoyagi, A., Ayodi, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavacos, I., Cesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Darmo, C., Ding, Y., Dinh, H., Divya, K.,
Braper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C., A., Falls, T., Fen, G.,
Fernandez, S., Finley, M., Flaggi, N., Forbes, L., Foster, M.,
Fraser, C.M., Gabisi, A., Ganta, R., Garner, T., Garza, M.,
                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 http://www.sanger.ac.uk/RGPChri0
RP11-108B14 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For there details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-108B14 The true left end of clone RP11-57366 is at 131459 in this sequence. The Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG 09-MAY-2003
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rattus norvegicus clone CH230-7118, WORKING DRAFT SEQUENCE, 2
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 TACAGTATTATAATGAGAACTACATGAGGCATACGGGTGAGGGGG 114
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/evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-11.1"
158682. .159170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DN
/db_xref="taxon:9606"
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HTG; HTGS_PHASE1; HTGS_DRAFT; I
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-108B14"
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Submitted (19-MAY-2013) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON MAY 9, 2003 this sequence version replaced gi:24941115.

The sequence in this assembly is a combination of BAC based reads and whole genome shockun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads Both sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, R., Halwes, S., Hadun, S.L., Hodgoon, A., Hegues, M., Jackson, L., Jacob, L., Jang, H., Johnson, R., Jolivet, A., Karpethy, S., Kally, S., Khan, S., King, L., Kovar, C., Liu, Jackson, H., Levan, J., Lewis, L., Liu, M., Mahlman, H., Levan, J., Lewis, L., Liu, M., Mahlman, M., Mahloy, K., May, J., Maheshwari, M., Mahlmartne, M., Mahloy, K., May, J., Maheshwari, M., Mahlmartne, M., Mahloy, K., May, J., Mahloy, K., May, J., Mahloy, K., May, J., Mahloy, K., May, J., Mahloy, S., McLeod, M. P., McMeill, T.Z., Meenen, E., May, J., Mahloy, S., McLeod, M. P., McMeill, T.Z., Meenen, E., Mahloy, K., Martin, K., Mahloy, K., Martin, K., Mahloy, K., Manja, B., Mahloy, K., Martin, K., Mahloy, K., Martin, K., Mahloy, K., Manja, B., Mahloy, K., Martin, K., Mahloy, K., Manja, B., Mahloy, K., Polad, M., Nortis, S., Parks, K., Paseerak, S., Pand, H., Perez, L., Robe, M., Rose, M.,
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Direct Submission
Submitted (16-SEP-2001) Human Genome Sequencing Center, Department
Of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 245135)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: CH230-7118
------ Summary Statistics
Assembly program: Atlast
Consensus quality: 222422 bases at least
Consensus quality: 232796 bases at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
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Direct Submission
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98697 AGAATCTAAATTAATTAATTAATGTAAATTTGATTACATATTTATGTATTATTAT 98756
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Best Local Simil
Matches 47; C
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                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX640454 165038 bp DNA linear VRT 20-MAY-2004 Zebrafish DNA sequence from clone CH211-1A19 in linkage group 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Actinopterygii, Neopeerygii, Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

    (bases 1 to 165038)

                           Estimated insert size: 242725; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ACTTAGGGAGGGGAAGAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTATT
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                                                                                                                                                                                                                                                                                                                                                1 242788: contig of 242788 bp in length
19 242888: gap of unknown length
19 245135: contig of 2247 bp in length.
Location/Qualifiers
1. 245135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 34; Indels
quality: 235239 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 TITATACAGIATTATAATGAGAACTACATGAG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="taxon:10116"
/clone="CH230-7118"
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241315. .242788
/note="wgs_contig"
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BX640454
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Unity a summarto. Vertinap as described abover.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) = 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr.: TREMBL; Wp:, WORNPEP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived zebrafish pUC subclones occasionally display inconsistency over the length of monouncleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-1A19
is from a CHORI-211 BAC library
VECTOR: pTARBAC2.1.
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Pred. No. 52;
0; Mismatches 16; Indels
only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
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74.6%;
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Query Match
Best Local Similarity 62.09
watches 57; Conservative
32.534
126176
126176
126176
183112
646358
646358
1003
1003
66788
6778
305491
305491
3399
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(91772
               TYPE: DNA
ORGANISM: Human
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US-09-586-935-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 824, App
Sequence 542, App
Sequence 3; Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 10, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Appl
Sequence 15859, A
Sequence 15255, A
                                                     July 22, 2005, 05:35:22; Search time 132 Seconds (without alignments) 1561.901 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 79207, A
Sequence 1, Appli
Sequence 15473, A
                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                         Issued Patents NA:*

(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-507-455-1
US-09-949-016-15381
US-09-734-674-3
US-09-949-016-13385
US-09-949-016-13386
US-09-949-016-13386
US-09-949-016-13386
US-09-949-016-13386
US-09-949-016-3386
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US-09-949-016-15255
US-09-949-016-79207
US-08-468-557-1
US-09-949-016-15473
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US-09-673-395A-542
US-09-368-588-3
US-07-854-596B-4
US-08-450-905B-15
US-07-982-759F-15
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                                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                                                                                                               1202784 segs, 818138359 residues
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                                                                                                                                                                                                        Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        - nucleic search, using sw model
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length: 2000000000
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450395
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Match
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25.6
25.6
25.2
25.2
25.2
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Perfect score:
                                                                                                                                                                                Minimum DB seq
Maximum DB seq
                                                                                                                        Scoring table:
                                        OM nucleic
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                                                                                                         Sequence:
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                                                        Run on:
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NG-09-99-016-15568, Application US/09949016

Sequence 15568, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                               Sequence 17550, A
Sequence 11420, A
Sequence 43, Appl
Sequence 16179, A
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41, Appl
41, Appl
1, Appli
37, Appl
12705, A
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                              Sequence 133
Sequence 161
Sequence 161
Sequence 17,
Sequence 11,
Sequence 41,
Sequence 41,
Sequence 41,
Sequence 11,
Sequence 11,
Sequence 11,
Sequence 11,
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Sequence 1
Sequence 1
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US-09-248-796A-1014
US-09-949-016-13359
US-09-949-016-16137
US-09-949-016-16138
US-09-949-016-15725
US-09-949-016-15725
US-09-949-016-15725
US-09-949-016-15725
US-09-949-016-15725
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US-09-949-016-17505
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US-09-949-016-17507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SSOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 15568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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Patent No. 6191267
GENERAL INFORMATION:
APPLICANT: KONG, HUIMIN
APPLICANT: HIGGINS, LAUREN S.
APPLICANT: DALTON, MICHAEL
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1 CATAGACTTAGGGAGGGCCAAGAAAAAATCCTCGAAAATTATTAAATATACATTTGATT
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| Sequence 2, Application US/08507455 |
| Patent No. 569561 |
| GENERAL INFORMATION: |
| APPLICANT: | TITLE OF INVENTION: |
| BIFUNCTIONAL EXPRESSION SYSTEM |
| INFORMERSEE: | NINON WE VANDERHYE P.C. |
| STREET: | 1100 NORTH GLEBE ROAD, | 8TH FLOOR |
| COUNTRY: USA |
| INFORMET: | USA |
| INFORMATION OF COMPATION |
| COUNTRY: USA |
| INFORMATION OF COMPATION |
| CONDUTER READABLE FORM: |
| MEDIUM TYPE: | Floppy disk |
| COMPUTER ISADABLE FORM: |
| MEDIUM TYPE: | POPPY |
| COMPUTER ISADABLE |
| COMPUTER PRADABLE |
| COMPUTER |
| POPENATION OF SYSTEM: |
| POPENATION OF SYSTEM: |
| APPLICATION NUMBER: US/08/507,455 |
| PILING DATE: 08-SEP-1995 |
| PILING DATE: 26-PEB-1995 |
| PILING DATE: 26-PEB-1995 |
| ATTORNEY FORMET INFORMATION: |
| REGISTRATION NUMBER: GB 9303988.1 |
| PILING DATE: 26-PEB-1993 |
| ATTORNEY FORMET INFORMATION: |
| REGISTRATION NUMBER: 29,009 |
| REFERENCE/DOCKET NUMBER: 29,009 |
| REFERENCE/DOCKET NUMBER: 1993 |
| REFERENCE/DOCKET NUMBER: 1993 |
| REFERENCE/DOCKET NUMBER: 1996 |
| REFERENCE/DOCKET NUMBER: 1996 |
| REFERENCE/DOCKET NUMBER: 29,009 |
| REFERENCE/DOCKET NUMBER: 1996 |
| REPROBREMENTER FOR SEQ ID NO: 2: |
| REGISTRATION NUMBER: 1996 |
| REFERENCE CHARACTER FOR SEQ ID NO: 2: |
| REGISTRATION NUMBER: 1996 |
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| REFERENCE CHARACTER FOR SEQ ID NO: 2: |
| REGISTRATION NUMBER: 1996 |
| REGISTRATION NUMBER:
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668..673
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550..555
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574..579
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692..697
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1411..1412
        misc_recomb
546..547
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635..636
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1035..1036
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US-08-507-455-2/c
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LOCATION:
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US-08-507-455-1
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APPLICANT: KUCERA, REBECCA B.
APPLICANT: SCHILDKRAUT, IRA
TITLE OF INVENTION: Cloning And Producing The N.BstNBI Nicking Endonuclease
FILE REPERENCE: NBB-178
CURRENT APPLICATION NUMBER: US/09/586,935
CURRENT FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 2.0
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 GGCAAGAAAAATCCTCGAAAATTATTAAATATATACATTTGATTTTTATTATACAGTA
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COUNTRY.

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/507,455

FILING DATE: 08-SEP-1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: GB 9303988.1

FILING DATE: 26-FEB-1993

ATTOMEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BIFUNCTIONAL EXPRESSION SYSTEM NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE:
                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,009
REFRENCE/DOCKET NUMBER: 1498-
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1619 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-507-455-1/c
; Sequence 1, Application US/08507455
; Patent No. 5695961
; GENERAL INFORMATION:
APPLICANT:
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.39
                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1)..(903)
US-09-586-935-4
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LENGTH: 906
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SEQ ID NO 13384
LENGTH: 38559
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Sequence 15381, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPRENEUE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03

SOFTWARE: FREEEE SAGEOF OF WINDOWS VERSION 4.0

SEQ ID NO 15381

LENGTH: 43333
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     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17201 TATAAAATAAAAAATTAGCC 17222
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Best Local Similarity 60.0%;
Matches 57; Conservative C
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Best Local Similarity 63.44
Matches 52, Conservative
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546..547
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635..636
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1411..1412
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1035..1036
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-15381
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NAME/KEY:
LOCATION:
                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                             NAME/KEY:
COCATION:
US-08-507-455-2
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                                                                                                                                                                                  FEATURE:
NAME/KEY:
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RESULT

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Sequence 13384, Application US/09949016

Sequence 13384, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

PAPLICANT: VENTER, U. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOL1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: FRESESE for Windows Version 4.0
Sequence 3, Application US/09734674

Patent No. 6498022

GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISCLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLO01018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 202001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ATAGACTTAGGGAGGGCAAGAAAAAAATCCTCGAAAATTATTAAATATACATTTGATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 202001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
26.7%; Score 33.6; DB 4; Length 20
Best Local Similarity 61.4%; Pred. No. 14;
Matches 54; Conservative 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.5%; Score 33.4; DB 4; Best Local Similarity 60.4%; Pred. No. 11; Matches 55; Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191702 GGGGCATACACATACAATGGAACATTAT 191729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 GAGGCATACGGGTGAGGGGGAACATGAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1) ... (36559)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-13384
                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(202001)
COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-09-949-016-13384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
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TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 210:
US-09-453-702B-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NS-09-453-702B-210/c

Sequence 210, Application US/09453702B

Patent No. 6365723

GENERAL INFORMATION:

APPLICANT: Blattner, Frederick of the content of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blatch
Burland, v.-.
Perna, Nicole T.
Plunkett, Guy
OTHER INFORMATION: n = A, T, C or G
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.7%;
56.6%;
                                                                                                                ch 26.5%;
1 Similarity 60.4%;
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 56.6
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                         Query Match
Best Local Similarity
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                 , OLDER 111 US-09-949-016-13386
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Sequence 13386, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASLES ESUSES OF WINDOWS VETSION 4.0

SEQ ID NO 13386

LENGTH: 30559
                                                                                                                                                                                                                                                                             Sequence 13385, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
FOLVENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE DETECTION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-0-0-08
PRIOR PILING DATE: 2000-0-0-0-08
PRIOR PILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                              37928 rarrarrarccreraraarcreaagacree 37958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTTTTATACAGTATTATAATGAGAACTAC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(38559)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(38559)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-13386
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    62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                              61
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                                                                                           2 ATAGACTTTAGGGAGGGGCAAGAAAAATCCTCGAAAATTATTAAATATACATTTGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GCAAGAAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTATTTTTTATACAGTAT
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
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  Length 38559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: WORTEN: PC-DOS/WS-DOS
SOFTWARE: WORD PETECT
COURSENT APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INCREATION:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2625;
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                                               36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
DB 4;
                                                                                                                                                                                                                                           37928 TATTATTATCCTGTATAAATCTGAAGACTCC 37958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
Score 33.4; DB Pred. No. 11; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.4; DB; Pred. No. 13; 0; Mismatches
                                                                                                                                                                                            TATTTTTATACAGTATTATAATGAGAACTAC 92
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1242 CATAGAAATATCGAATGGGAAAAAAAACTGCATAAAAGGCATTAAAAAGGGGACGAAT 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CATAGACTTAGGGAGGGCCAAGAAAAATCCTCGAAAATTATTAAATATACATTTGATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CATAGACTTAGGGAGGGGCAAGAAAAAATCCTCGAAAATTATTAAATATACATTTGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 1309;
                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA ENCODING (LYS46, ASP97, ASP113) AND (LYS46, ASP113, ASP113) AND (LYS46, ASP113, ASP113) AND (LYS46, ASP113, ASP113) THAUMATIN I NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:
PILING DATE: 14-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 268,702
FILING DATE: 08-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOACHIM J.

TITLE OF INVENTION: DNA ENCODING (LYS46, ASP97, ASP113) AND TITLE OF INVENTION: THAUMATIN I (LYS46, ASP113, ASP113, THAUMATIN I (LYS46, ASP113, ASP113) THAUMATIN I (CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/407,416 FILING DATE: 14-SEP-1889 PRIOR APPLICATION DATA: APPLICATION NUMBER: 268,702 FILING DATE: 08-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
                                                                                                                                                                            Patent No. 5221624
; APPLICANT: BLAIR, LINDLEY C.;KODURI, JAR-HOW;WEICKMANN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.6%; Score 32.2; DE
Best Local Similarity 61.2%; Pred. No. 13;
Matches 52; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1182 TTTTTTTTAAAAATCTTAATAA 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1182 TTTTTTTAAAAATCTTAATAA 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TTATTTTATACAGTATTATAATGA 85
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US-09-023-655-824/c
S-09-023-655-824/c
; Sequence 824, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocke, Benjamin G.
                                                   1108 crrccarcrcaacccan 1092
       CATACGGGTGAGGGGGA 115
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Best Local Similarity 61.2%;
Matches 52; Conservative C
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; LENGTH: 1309
     66
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                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSESEQ for Windows Version 4.0
LENGTH: 1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1108 ATTTTAGTATATAAATTTGCTTTTTGTTTTATACAGAATATAAAGATTTCCCTCATTAAT 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60, Application US/09673395A
; Sequence 60, Application US/09673395A
; Patent No. 6210923
; GENERAL INFORMATION:
    APPLICANT: SPECHT, THOMAS
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHISTIAN
; APPLICANT: PILARSKY, AND SERVING APPLICANT: APPLICANT: PILARSKY, THISTIAN
; APPLICANT: AND SERVING AND SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
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Score 32.2; DB 4; Length 1 Pred. No. 12; 0; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/673,395A CURRENT FILING DATE: 2000-10-17 NUMBER OF SEQ ID NOS: 637 SOFFWARE: PATENTIN VEF. 2.1 SEQ ID NO 60
                                                                                                                                                  Sequence 4117, Application US/09949016
Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.6%;
Best Local Similarity 63.6%;
Matches 49; Conservative
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                                                                                                                             US-09-949-016-4117/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-4117
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APPLICANT: Susan G. Stuart
APPLICANT: Or INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
ADDRESSEROINDER: 1508
ADDRESSEROINDER: 1308 G. Competible
COMPUTE: 1808 G. Competible
ATTEREON: (650) 184-186
ATTEREON: (6
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Db 1217 ¢TTCCATĠTĠĀAĠĠĠTĀ 1201 Search completed: July 22, 2005, 08:41:12 Job time : 137 secs

99 CATACGGGTGAGGGGA 115

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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/DSO7_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4:: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USOB_PUBCOMB.seq:*
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                                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7173243 seqs, 3172129809 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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126
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		10000	מספרו דולודורות	Sequence	Sequence	Seguence 2	Sequence 2663, Ap	Sequence	Sequence	Sequence 166581,
SUMMARIES				21 US-10-764-581-17	JS-10-398-221-3339	3-09-764-877-2662	US-09-764-877-2663	JS-10-242-515-2662	JS-10-242-515-2663	JS-10-425-115-166581
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		Query	ביייים ביייי	126			6112	6112	6112	2084
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		0.00	2000	126	36.4	36	36	36	36	35.6
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5237 19 US-10-433-793-138 S 27587 11 US-09-997-722-253 S	35.2 27.9 3673778 16 US-10-312-841-2 Sequence 2	35 27.8 585 17 US-10-027-632-221497 Sequence 22	34.8 27.6 495269 17 US-10-398-221-8 Sequence 9, 34.8 27.6 3011208 17 US-10-398-221-2058 Sequence 2	5 34.4 27.3 7450 15 US-10-240-453-5 Sequence 5,	7 34.2 27.1 906 17 US-10-235-289-4 Sequence	34.2 27.1 5391 15 US-10-311-455-215 Sequence	0 34.2 27.1 8166 15 US-10-311-455-1765 Sequence	1 33.8 26.8 5489 15 US-10-311-455-2094 Sequence	2 33.8 26.8 15853 17 US-10-221-613-421 sequence	4 33.6 26.7 202001 9 US-09-734-674-3 Sequence	5 33.6 26.7 202001 14 US-10-274-990-3 Sequence	o 33.0 20.7 202001 24 US-11-01-025-3 Sequence 7 33.4 26.5 15373 15 US-10-311-455-440 Sequence	8 33.2 26.3 2000 9 US-09-938-842A-4553 Sequence	9 33.2 26.3 2000 11 US-09-938-842A-4553 Sequence	1 33.2 26.3 380963 22 US-10-737-082-5 Sequence	2 33.2 26.3 380963 22 US-10-765-790-5 Sequence	3 33 26.2 201 20 US-10-719-993-20393 Sequence	5 33 26.2 201 21 US-10-741-600-40227 Sequence	6 33 26.2 201 21 US-10-741-600-67698 Sequence	/ 33 26.2 /// 13 US-10-02/-532-32/41 Sequence	33 26.2 13784 17 US-10-257-166-144 Sequence	0 33 26.2 24438 20 US-10-719-993-7017 Sequence	1 33 26.2 24436 21 US-10-/41-000-1/939 Sequence 1/939, 26.2 1980090 20 US-10-719-993-6815 Sequence 6815,	33 26.2 1980090 21 US-10-741-600-17676 Sequence	32.8 26.0 6308 15 US-10-311-455-1444 Sequence 1444, 32.8 26.0 17869 15 US-10-311-455-77 Sequence 77, Ap	. ALIGNMENTS	RESULT 1 US-10-764-581-17 US-10-764-581-17 Sequence 17, Application US/10764581 Publication No. US20050032086A1 GENERAL INFORMATION: TITLE OF INVENTION: IMPROVED METHODS OF RNA AND PROTEIN SYNTHESIS FILE REFERENCE: B4949AB CURRENT APPLICATION NUMBER: US/10/764,581 CURRENT FILING DATE: 2004-01-27 PRIOR APPLICATION NUMBER: PC1/2P PRIOR FILING DATE: 2002-07-26 PRIOR FILING DATE: 2001-07-27 NUMBER OF SEQ ID NOS: 17 SOFTWARE: Patentin version 3.1 LENGTH: 126 TYPE: DNA OBCANISM: Bacillus stearcthermophilus US-10-764-581-17 Query Match Best Local Similarity 100.0%; Pred. No. 3.8e-20; Matches 126; Conservative 0; Missmatches 0; Indels 0; Gaps
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TTATTTTTATACAGTATTATAATGAGAACTACATGAGGCATACGGGTGAGGGGAACATG 120
                          61 TIATITITATACAGTATTATAATGAGAACTACATGAGGCGTACGGGTGAGGGGGGGAACATG 120
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US-10-389-221-3339/c
US-10-398-221-3339/c
| Sequence 3339, Application US/10398221
| Publication No. US20040018514A1
| GENERAL INFORMATION:
| APPLICANT: KUNST, Federik
| APPLICANT: GLASER, Philippe
| TILLE OF INVENTION: Listeria innocua, genome and applications
| FILLE REPERENCE: 344 702 - US
| FILLE REPERENCE: 2003-03-27
| PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
| PRIOR APPLICATION NUMBER: FR 00/12 697
| PRIOR APPLICATION NUMBER: FR 00/12 697
| PRIOR FILING DATE: 2000-10-044
| NUMBER OF SEQ ID NOS: 4025
| SOFTWARE: PatentIn version 3.0
| SEQ ID NO 3339
| LENGTH: 2121
| LENGTH: 2121
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28.9%; Score 36.4; DB 17; Length 2121;
Best Local Similarity 59.8%; Pred. No. 70;
Matches 61; Conservative 0; Mismatches 41; Indels 0;
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Batent No. US20020147140A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIN Ver. 2.0
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NAME/KES:

A:
IOCATION: (1)..(end)

OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u US-10-398-221-3339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2662
                                                                                            121 ATGAAC 126
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LENGTH: 6112
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2667 GGADADADAGAGAGTACACTAACACGACTAATAAATTTATATTTGTATAAATGTACCCTAT 2608
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ITILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies ITILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies ITILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERBYCE: PC005C1
CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR PILING DATE: 2000-09-11
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR PILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR PILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT PILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6112;
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                                                                                                                                           2607 TATTTTAAGAATTATATAATGAATACTGATAA 2576
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                                                                                      78 TATAATGAGAACTACATGAGGCATACGGGTGA
                                                                                                                                                                                                                                                                                            ; Sequence 2663, Application US/09764877; Patent No. US20020147140A1; GENERAL INFORMATION:
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Publication No. US20040009488A1
GENERAL INFORMATION:
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62.0%;
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Best Local Similarity 62.04
Matches 57; Conservative
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ORGANISM: Homo sapiens
US-09-764-877-2663
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US-09-764-877-2663/c
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                             Length 6112;
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                                                                                                                                                                                                                     Query Match 28.6%; Score 36; DB 17; Best Local Similarity 62.0%; Pred. No. 1.1e+02; Matches 57; Conservative 0; Mismatches 35
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                                                                  TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-2662
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SEQ ID NO 2662
LENGTH: 6112
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RESULT 7 US-10-425-115-166581/c

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Sequence 166581, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Low, Vinhus
APPLICANT: Cao, Vongwei
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 166581
LENGTH: 2084
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Publication No. US20040142334A1
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 138
LENGTH: 5237
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-433-793-138
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28.3%; Score 35.6; DB 20; Length
Best Local Similarity 64.6%; Pred. No. 1.1e+02;
Matches 53; Conservative 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_83501C.1
US-10-425-115-166581
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ORGANISM: Artificial Sequence
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Best Local Similarity 67.6*
Matches 50; Conservative
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US-10-027-927-22497/C

Sequence 221497, Application US/10027632

Publication No. US2003020407549

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

FRIOR FILING DATE: 2000-07-12

FRIOR FILING DATE: 2000-07-20

FRIOR PAPLICATION NUMBER: US 60/198,676

FRIOR PAPLICATION NUMBER: US 60/193,483

FRIOR PAPLICATION NUMBER: US 60/185,218

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 1200-03-29

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-08-08

FRIOR FILING DATE: FASESQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ NUMBER OF SEQ ID NOS: 325720
SECTAMARE: PARLED FOR WINDOWS VERSION 4.0
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Best Local Similarity 64.99
Watches 50; Conservative
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Best Local Similarity
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ORGANISM: Human
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SEQ ID NO 221497
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Publication No. US20030186277A1

Publication No. US20030186277A1

APPLICANT: Epigenomics AG

TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC

TITLE OF PRERENCE: BO1/1208/WO

CURRENT APPLICATION UMBER: US/10/312,841

CURRENT FILNG DATE: 2002-12-30

NUMBER OF SEQ ID NOS: 2
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827,129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%; Score 35.2; DB 16; Length 3673778; 60.4%; Pred. No. 7e+02; tive 0; Mismatches 38; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 27587;
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                 TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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7e+02;
38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.1%; Score 35.4; DB 11; Best Local Similarity 63.5%; Pred. No. 2.3e+02; Matches 54; Conservative 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ATTITIATACAGIATTATAATGAGAACTACATGAGG
                                                                                                                     PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR PELLING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 301
SOFTWARE: Patentin version 3.1
SEQ ID NO 253
LENGTH: 27587
                                          FILE REFERENCE: A-71171/RMS/DCF
CURRENT APPLICATION NUMBER: US/09/997,722
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7499 CCAAGGAATTCATGTGTAGGAAATC 7523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 ATGAGGCATACGGGTGAGGGGGAAC 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 60.4
Matches 58, Conservative
                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-09-997-722-253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-10-027-632-221497/c
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; LOCATION: (379615)
US-10-312-841-2
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                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                         14 AGGGGCAAGAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTATTACA 73
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                                                                                                                                                                                                                                                                                                                                                                              | Sequence 8, Application US/1039821
| Publication No. US20040018514A1
| SEMERAL INFORMATION:
| APPLICANT: KUNST, Philippe
| TITLE OF INVENTION: Listeria innocua, genome and applications
| FILE REFERENCE: 344 702 - US
| FILE REFERENCE: 344 702 - US
| CURRENT FILING DATE: 2003-03-27
| PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
| PRIOR PLLING DATE: 2000-10-04
| PRIOR PLLING DATE: 2000-10-04
| PRIOR PLLING DATE: 2000-10-04
| SOFTWARE: PatentIn Version 3.0
| SOFTWARE: PatentIn Version 3.0
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| Publication No. US20040018514A1
| GENERAL Involvation:
| APPLICANT: GLASER, Philippe
| TITLE OF INVENTION: Listeria innocua, genome and applications
| PILE REPERBNCE: 344 702 - US
| CURRENT APPLICATION NUMBER: US/10/398,221
| CURRENT APPLICATION NUMBER: PT/FR 01/03 061
| PRIOR APPLICATION NUMBER: FT 00/12 697
| PRIOR FILING DATE: 2000-10-04
| OFFICE OFF
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NAME/KEY: misc feature

LOCATION: (1)..(end)

OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
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                                                                                                                                       74 GTATTATAATGAGAACT 90
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Best Local Similarity 58.8%
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CRGANISM: Listeria innocua
US-10-398-221-2058
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LENGTH: 3011208
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GENERAL INFORTALION:

APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Transcription
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: Transcription
TITLE OF INVENTION: With DNA TRANScription
FILE REFERENCE: 5013.1009
CURRENT APPLICATION NUMBER: PCT/EP01/03973
FRIOR RILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: DE 10043826.1
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                                                                  Gaps
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27.6%; Score 34.8; DB 17; Length 3011208; ilarity 58.8%; Pred. No. 8.3e+02; Conservative 0; Mismatches 42; Indels 0; G
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Pred. No. 2.8e+02;
0; Mismatches 26;
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LOCATION: (4653, 5152, 5156..5157, 5159, 5722)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/10240453; Publication No. US20030148326A1
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27.3%;
Best Local Similarity 65.8%;
Matches 50; Conservative (
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Query Match
Best Local Similarity
Matches 60; Conserv
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/note="Vector: pBluescript SK plus; Site 1: EcoRI; Site 2: XhoI; The library was constructed by R Haywood. cDNAs were synthesized from ganetocyte poly(A)+ RNA by oligo d(T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="gametocyte (stage III-V)"
/lab host="DH10B (GeneHog, Invitrogen, Inc.)"
(Colone lib="Plasmodium falciparum 3D7 gametocyte cDNA
ibrary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Plasmodium falciparum 3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:36329"
28.7
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                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
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AUTHÒRS
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BM274717
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AL108124 BJ629764
CLI10320 ISBI-53F3
CF284280 AGENCOURT
BP721218 BP721218
BG143667 UE 58G07.x
CE073145 Ligr-988-AV207641
AV101294 AV101294
BU070396 im09f10.x
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BM310349 ihl1f02.x
BQ787408 im09f10.y
AL652174 AL652174
BZ322030 ia60c12.g
AL646926 AL646926
BX749863 BX749863
AL104814 Drosophil
BJ338343 BJ38843
BH645122 BOHUN84TR
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im09f10.y
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AL646926
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                                                                                                     catagacttagggaggggca......tgagggggaacatgatgaac 126
                                                                                                                                                            68479088
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                           34239544 seqs, 19032134700 residues
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                                                                                                                                                                                                  Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       sw model
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BP720714
BJ629764
CNS017JM
CL110320
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BP721218
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BU070396
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BQ787408
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BZ322030
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CE073145
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CNS014ZO
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BH645122
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Gapop 10.0 , Gapext 1.0
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                                       nucleic search, using
                                                                                                                                                                          seq length: 0
seq length: 200000000
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9b_htc:*

9b_est4::*

9b_est4::*

9b_9s81:**
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BM274717
PfESTOa73103.yl Plasmodium falciparum 3D7 gametocyte cDNA library Plasmodium falciparum 3D7 cDNA 5' similar to TR:077380 077380 PFC0780W PROTEIN. ;, mRNA sequence.
CR314707 Medicago
BG60216 EST501506
BG7008596 coe144c05.
BH440605 BORNN16TR
CG971096 MBEDF69TR
CG971096 MBEDF69TR
CD268594 taa96c04.
BJ332409 BJ332409
BJ332409 BJ332409
BJ332567 BJ332567
BJ332567 BJ332567
BJ332567 BJ332567
BJ332567 BJ333899
CR313043 Medicago
CR313043 Medicago
CR313043 Medicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Library was constructed by R. Haywood. DNA sequencing by:
Library was constructed by R. Haywood. DNA sequencing by:
Library was constructed by R. Haywood. DNA sequencing obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: L. David Sibley
WashU Plasmodium EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
    CR314707
BG602416
BH440605
CC971096
CC371096
CC3712409
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BX132409
BX1323409
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CX313043
CC8113309
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168 TTAAAAATTTGGATTATTTGATCATAATGGAGTCTATGGGAGACGG 123
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priming, size-selected and directionally cloned into the BCORi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the ExAssist helper phage (Stratagene), the phagemid using the ExAssist helper phage (Stratagene), the phagemid using the ExAssist with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells. Clone Availability: David Sibley, Washington University."
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1 (bases 1 to 462)
08ada, S., Kitayama, A., Ueno, N. and Taira, M.
Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP735538 Osada Taira anterior neuroectoderm (ANE) pCS105 cDNA library Xenopus laevis cDNA clone XL505\times03\times0, mRNA sequence. BP735538
                                                                                                                                                                                                                                                                                        20 AAGAAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTATTTTTTATACAGTATTA
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                                                                                                                                                                                                                                                      Gaps
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/tissue type="anterior neuroectoderm"
/dev_stage="late gastrula (stage 12.5)"
/clone lib="0sada Taira anterior neuroectoderm (ANE)
pCS105_cDNA library"
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                                                                                                                                                                                                             30.8%; Score 38.8; DB 4; Length 266;
larity 67.1%; Pred. No. 62;
Conservative 0; Mismatches 27; Indels
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Pred. No. 59;
0; Mismatches 42; Indels
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URL:http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.
Location/Qualifiers
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Contact: Masanori Taira
Department of Biological Sciences
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/db_xref="taxon:8355"
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1 Similarity 60.4%;
64; Conservative
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                       Vaces, I.C. 1.0. 1.0. N. and Taira, M. Sada, S. Kitayana, A. Kitayana, A. Uso, N. and Taira, M. Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos Unpublished (2004)
                       BP720714 Osada Taira anterior neuroectoderm (ANE) pCS105 cDNA library Xenopus laevis cDNA clone XL447b2lex 3', mRNA sequence.
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Graduate School of Science, University of Tokyo; CREST, Japan
Graduate School of Science, University of Tokyo; CREST, Japan
Science and Technology Corporation, Japan
7-3-1 Hongo, Buhkyo-ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Email: m_taira@blol.s.u-tokyo.ac.jp,
URL:http://www.shigen.nig.ac.jp/hbrp/xenopus/est/.
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/dev stage="late gastrula (stage 12.5)"
/clone_lib="09ada Taira anterior neuroectoderm (ANE)
pCS105 CDNA library"
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  479 bp
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/clone="XL447b21ex"
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60.4%;
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1134 bp DNA linear GSS 05-JAN-2004 ISB1-53F3 Sp6.1 ISB1 Xenopus tropicalis genomic clone ISB1-53F3, genomic survey sequence.
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                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia; Pipoidea, Pipidae; Xenopodinae; Xenopus, Silurana.

1 (bases 1 to 1134)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T., Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
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Washington University School of Medicine
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Xenopus tropicalis
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/mol_type="genomic DNA"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seg primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC end
High quality sequence start: 77
High quality sequence stop: 249.
Location/Qualifiers
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clone lib="ISB1"
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                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL162k22"
/tissue type="whole embryo"
/dev_stage="stage 10.5"
/clone lib="NIBB Mochii normalized Xenopus early gastrula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23.JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d' Stude du Polymorphisme Hummain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 CTTAGTGTGGATCAAGTACAAGGTACTGTTTAATTATTACAGAGAAAATGAAATCATTT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence SP6 end of BAC BAC BAC 3D12 of DrosBAC library from Drosophila melanogaster (fruit AL108124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 CTTAGGGGGGGCGAAGAAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTATTT
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 110)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 TTAAAAATTTGGATTATTTGATCATAATGGAGTCTATGGGAGACGG 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38.8; DB 4;
Pred. No. 59;
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches

    .497
    organism="Xenopus laevis"

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/db_xref="taxon:7227"
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/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="BACN37D12"
/clone_lib="DrosBAC"
                                                                                                                                                                                                   http://xenopus.nibb.ac.jp.
Location/Qualifiers
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1 Similarity 60.4%;
64; Conservative
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Matches 64; Conserv
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

COMMENT

source

ORIGIN

FEATURES

RESULT 5 CNS017JM/c

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Gaps

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Query Match
Best Local
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BG143667
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            SM Xenopus lacetis Antican Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Kenopodinae; Xenopus; Xenopus.

I (bases 1 to 792)
SINH-MG http://mgc.nci.nih.gov/.

I (bases 1 to 792)
SINH-MG http://mgc.nci.nih.gov/.

I (bases 1 to 792)
Outional Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg: 31 Ranbon? Betheeda, MD 20892
Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAMJ252 row: 1 column: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="DH10B phage-resistant)"
/clone lib="MUCHD XGC_Spl"
/note="Organ: spleen; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Avertage insert size 2.4 kb. Constructed by Life
Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus, Kenopus.

1 (basea 1 to 312)
Osada, S., Kitayama, A., Ueno, N. and Taira, M.
Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 CTTAGGGAGGGGCAAGAAAAAATCCTCGAAAATTATTAAATATACATTTGATTTTATTT
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Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan
Science and Technology Corporation, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 TTATACAGTATTATAATGAGAACTACATGAGGCATACGGGTGAGGG 112
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Xenopus laevis (African clawed frog)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:5507094"
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EST 01-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTS: ut58907.y1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
MGI:1076336
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                              /tissue_type="anterior neuroectoderm"
/dev.stāge="late gastrula (stage 12.5)"
/clone_lib="Osada Taira anterior neuroectoderm (ANE)
pcs105_cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 bp mRNA linear EST 01-
ULS8g07.x1 Soares mouse_NMGB_bcell Mus musculus cDNA clone
IMAGE:3332172 3', mRNA sequence.
BG143667
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                                                                                                                                                                                                                                                                                                                                                                                   Length 312;
                  Tel: 81-03-5841-4434
Fax: 81-03-5841-4434
Email: m_taira@biol.s.u-tokyo.ac.jp,
URL:http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 5; I
Pred. No. 1.6e+02;
0; Mismatches 44;
                                                                                                                                                     /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL448n2lex"
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Location/Qualifiers
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l Similarity 58.1%;
61; Conservative 0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (base 1 to 309)

Ex Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishiikawa, T., Itoh, M., Izawa, M., Radota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, M., Miki, M., Sato, K., Shibata, K., Shigemoto, Y., Shiraki, T., Sogabe, Y., Shibata, K., Sulaki, H., Takahashi, F., Tateno, M., Tominaga, N., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshino, H., et al. 1999)

U Onpublished (1999)

Contact: Yoshihide Hayashizaki
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M. Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Okazaki, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Akibata, Y., Muramatsu, M., Automated filtration-based high-throughput plasmid preparation system. Genome Res 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki.w. Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp)
further details.
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/clone="1700096D08"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dev stage="adult"
|lab_host="SOLR"
                             Mus musculus (house mouse)
Mus musculus
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                       39 ATTATTAAATATACATTTGATTTTATTTTATACAGTATTATAATGAGAACTACATGAGG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis. I (bases 1 to 635)
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
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Colone_lib="bog_Library"
/note="%2ite_l: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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                          Score 37; DB 4; Length 542;
Pred. No. 1.5e+02;
); Mismatches 25; Indels
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                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kirkness EF
The Institute for Genomic Research
Department of Bukaryotic Genomics,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="Standard Poodle"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic survey sequence.
                                                                                                                                                                                                                                                   99 CATACGGGTGAGGGGA 115
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CE073145.1 GI:35136760
                                                                                                                                                                                                                                                                                                     109 CTTTCATGGGAAGGGGA 125
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Canis familiaris
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                       ch 29.4%;
I Similarity 67.5%;
52; Conservative
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Fax: 301-838-0208
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/clone lib="RIKEN full-length enriched, adult male testis" /note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Nouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                    GAGAGAGAGGAGCTCTTTTTTTTTTTVN 3'], cDNA was grepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                             RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
                                                                                                                                                                                                                                                                                                                                                 Gaps
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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457 bp mRNA linear EST 03-JAN-2002 ihl1f02.y1 Human insulinoma Homo sapiens cDNA 5', mRNA sequence. BM310085.1 GI:18042909
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Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Mecabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to ppluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 GAATTCCTCAAGGGACAGAAAAAAATTGGAGACTGTTGAAATGCAGATTGGAAGTAAT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
im09f10.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6034699
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Ilmilier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williama, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Whilsima, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Unpublished (200)
Chrer Estra: Imoglafio, Y. Consortium
Endocrine Pancreas Consortium
Endocrine Pancreas Consortium
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                                                                                                                                               BU070396.1 GI:22511585
                                                                                                                                                                                                                                           Homo sapiens (human)
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                                                              mRNA sequence.
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Transcriptional sequencing A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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              39 ATTATTAAATATACATTTGATTTTATTTTTATACAGTATTATAATGAGAACTACATGAGG 98
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clone lib="Mus musculus C57BL/6J ES cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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/cell type="ES cell"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                               204 CTTTCATGGGAAGGGGAATA 185
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Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Chie Owa
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yo23a07.r1 Soares adult brain N2b5HB55Y Homo sapiens CDNA clone
IMAGE:178740 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University protocol. (http://genome.wustl.edu/est/lambda_protocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Buclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 617-495-8557
Email: dmelton@bioth.harvard.edu
Email: dmelton@bioth.harvard.edu
Email: dmelton@bioth.harvard.edu
Email: dmelton@bioth.harvard.edu
Dr. J. Ferrer In vivo mass-excised to
pBluescript Sk- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibon
High quality sequence stop: 377.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tiseue type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="Human insulinoma"
/note="Cogan: pancreas; Vector: pBluescript SK-; Site_1:
Xho1; Site_2: EcoR1; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 GAATTCCTCAAGGGACAGAAAAAAAAATTGGAGACTGTTGAAATGCAGATTTGAAGTAAT 356
                                                                                                                                                                                                                                                                                                                                                                                                                        Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                      Bukaryogica, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases I to 457)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hiller, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Cardenas, M., Titter, E., Ronko, I., Bennett, J., Williams, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Milliams, T., Jackson, Y. and Bowers, Y.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium
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.larity 63.6%; Pred. No. 1.7e+02;
Conservative 0; Mismatches 32; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
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High quality sequence stops: 327
Source: IMAGE Consortium, LLNL
This clone is avallable royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 442 Std Brror: 0.00
Seq primer: M13R91
High quality sequence stop: 327.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 459)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,B., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                     Contact: William RK
Contact: Willean RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.8; DB 7; Length 459;
Pred. No. 1.7e+02;
0; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'dev stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 Tritriaaaararrarrarggerrerge 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3840936"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 TITIATACAGTATTATAATGAGAACTAC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:178740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: July 22, 2005, 08:38:52 Job time : 3142 secs
                                                                                                                                   The WashU-Merck EST Project Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 56; Conserv
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This Page BIGTAR (USBIG)

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